

Population-specific expression of antimicrobial peptides conferring pathogen resistance in the invasive ladybird *Harmonia axyridis*

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Supplementary Table and Figures

Table S1. List of 23 gene-specific primer pairs used for AMP gene expression analysis (22 AMPs and RPS3 as housekeeping gene for normalization of qPCR data).

Figure S1. The *col1* gene sequence with the corresponding binding sites for dsRNA and qPCR primers.

Figure S2. Kaplan-Meier survival curves for dose-dependent survival of water-injected beetles after injection with different concentrations (8×10^3 cfu/ml, 8×10^5 cfu/ml, 8×10^7 cfu/ml, 8×10^9 cfu/ml) of *P. entomophila* (Pe) or with PBS as a control (n = 10 per treatment).

Figure S3. Verification of the normality assumption for the AMP gene expression analysis data. Assumption was verified per gene by comparison of the t-quantile-quantile plot for standardized residuals of the ANOVA model (red graph) with t-quantile-quantile plots for 11 simulated, truly t-distributed data sets with equal sample size (black graphs). Genes: a) Attacin4, b) Attacin6, c) Attacin10, d) Attacin18, e) Coleopteracin1, f) Coleopteracin5, g) Coleopteracin8, h) Coleopteracin-likeA, i) Coleopteracin-likeB, j) Coleopteracin-likeC, k) Coleopteracin-likeD, l) C-type Lysozyme1, m) C-type Lysozyme2, n) C-type Lysozyme3, o) C-type Lysozyme4, p) Defensin1, q) Defensin3, r) Defensin7, s) Sapecin-like Defensin7, t) Thaumatin1, u) Thaumatin2, v) Thaumatin4.

Supplementary Files

File S1 R-Script for AMP gene expression analysis

File S2 qPCR data for AMP gene expression analysis

File S3 qPCR data for Col1-RNAi knockdown verification

File S4 Survival data

Table S1

Primer	Target gene	Sequence forward (5'-3')	Sequence reward (5'-3')
Att4	Attacin4	CAAGAATCCAGGAGGTACTCAAG	ACCGCCTCCTAATGTTGTTG
Att6	Attacin6	AAGAATCCAGGAGGTACACAGG	ACCGCCTCCTAATGTTGTTG
Att10	Attacin10	CGCTTTAGCCTCTTCAGAATCA	TCCTTTATGCCCCAAAGTCA
Att18	Attacin18	ACCCACAAGGTACGCAGGT	CCTCCTCCTAATGCTGTTGG
Col1	Coleopteracin1	CTGCATCTCCTTCCAATATGC	GGTCCTTCGGGAACAACATA
Col5	Coleopteracin5	CATTTGCCTGCATTTACTTCC	TTGGGGCTCCAGGTAGAAG
Col8	Coleopteracin8	GGAAGAGGTTGTTGTAGATGGAG	TCTGGTGAGTGATGGGTCAA
ColLA	Coleopteracin-likeA	GAAGGATGGCAAGTCGAACA	ACCACGTGAAGGTTCTCCT
ColLB	Coleopteracin-likeB	AGATGTGCCTTGCTTCGAGA	ATTGTGCGAGAACCACCAAC
ColLC	Coleopteracin-likeC	CATGTTCGGGACTCTGAAGG	CTCACAGATCCGGCAGTGTT
ColLD	Coleopteracin-likeD	CACGTTCTGGGATACTGATGG	CACCTGAAGGTTGCTCCAAG
CLys1	C-type Lysozyme1	GCGTTTGTGCAGAGAAGGTC	TAACATGGCGGAAGTGGAAG
CLys2	C-type Lysozyme2	TCAAAGCTTGGAATGGTTGG	TCCATCAACATAGCGGCATT
CLys3	C-type Lysozyme3	GGGAATTCCAGGCAATCAGT	CATGGCAACCTTTACCAGGA
CLys4	C-type Lysozyme4	GGGTCAGAAGCCCGAATTTA	CAGCGGTGTCAAAGTTGGAT
Def1	Defensin1	CATTCTCCTCTCCTACCGAACC	GGCGACACAATGTAATGCAC
Def3	Defensin3	ACCGAAAGGGGAAATTCTTC	GGCGACACAATGTAATGCAC
Def7	Defensin7	TGAGTATCGAAGCAGGAACCA	TCCTCCCTCGTAGTTGAAGG
SapL7	Sapelin-like Defensin7	ACCGAACCGAAAGAGGAAAT	GCAGCTTAAAGCACATGCAG
Thau1	Thaumatococcus1	TTCTGGGGAAGAAGTTGGTG	CTCGACAAGGGTAGCTGGAG
Thau2	Thaumatococcus2	TGAAGGTGGACAAGTGTGGA	CAGGGGCATAAACAGAGACC
Thau4	Thaumatococcus4	AGGGCTGGACTTCTACGACA	TCCTGGACAATGGTTGTTGA
RPS3	Ribosomal protein RPS3	GGCTACCAGAACCGACAGAG	GTGCTATGGCGCATAATCCT

Figure S1

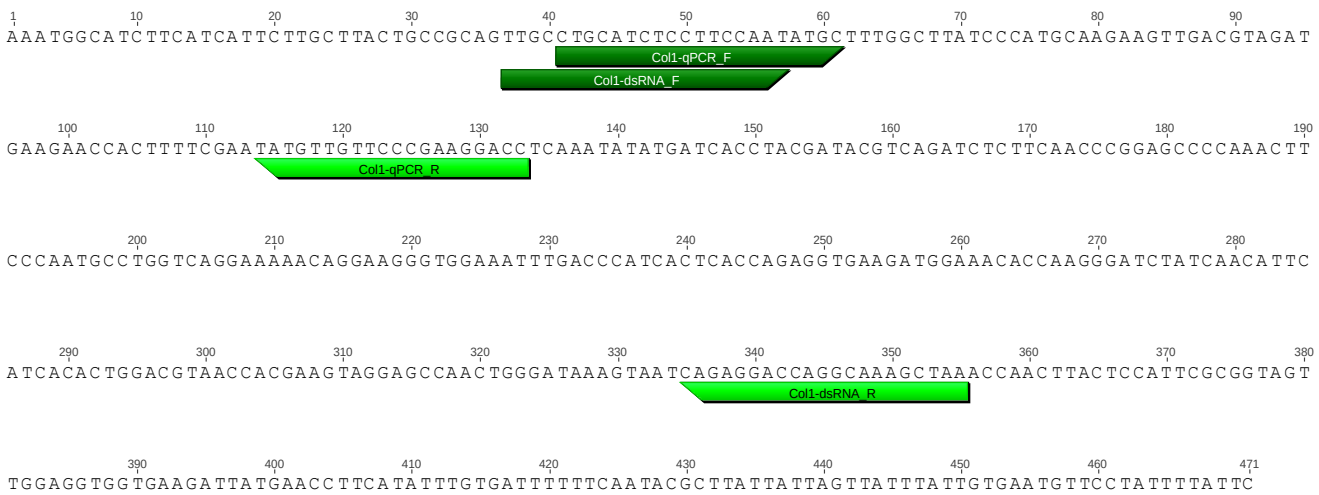


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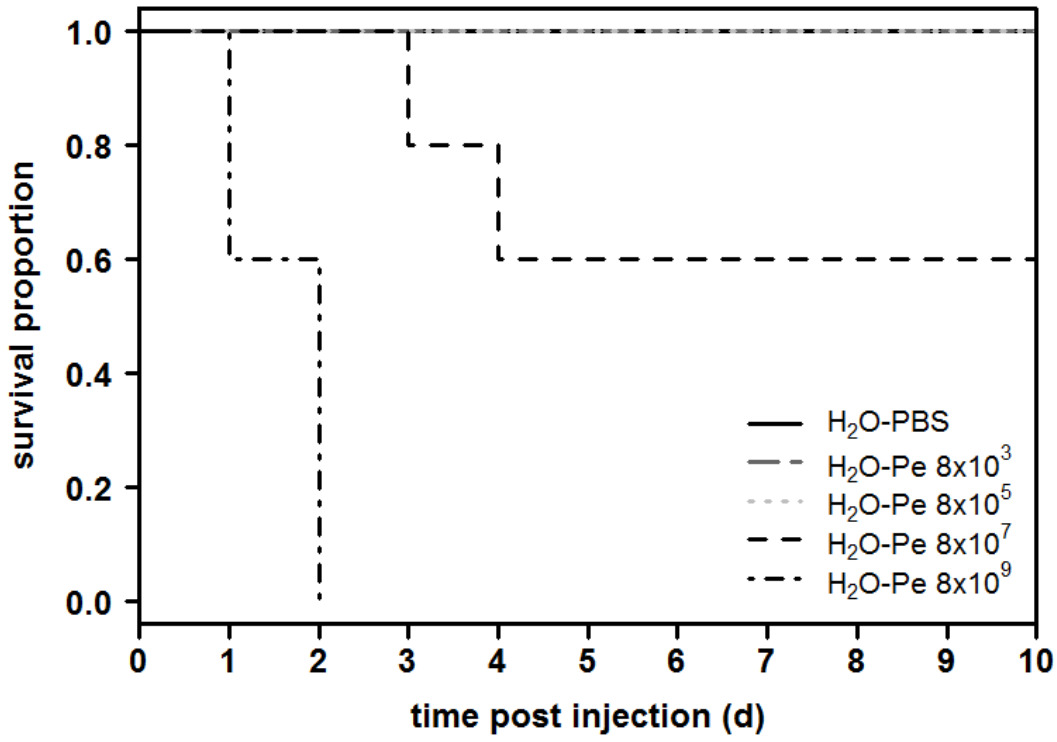


Figure S3 a

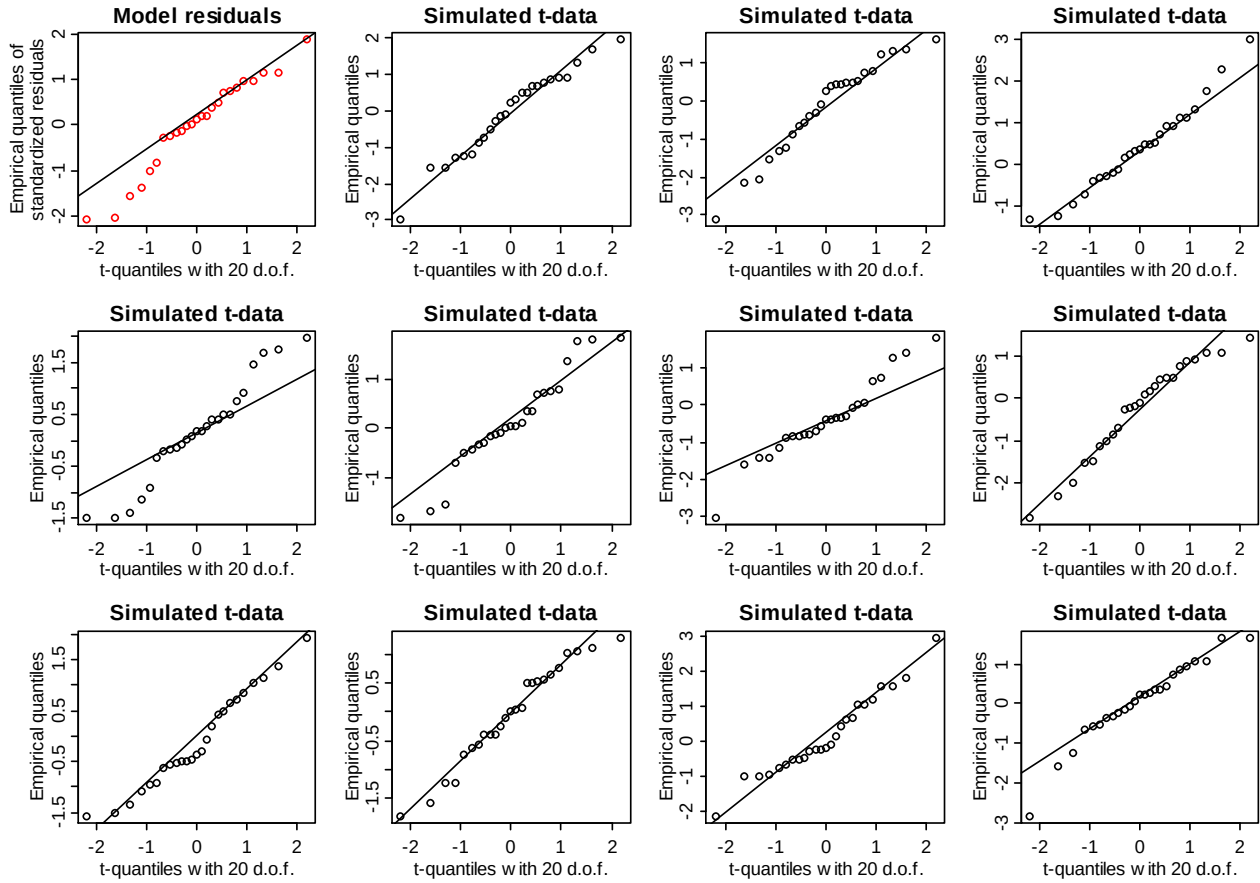


Figure S3 b

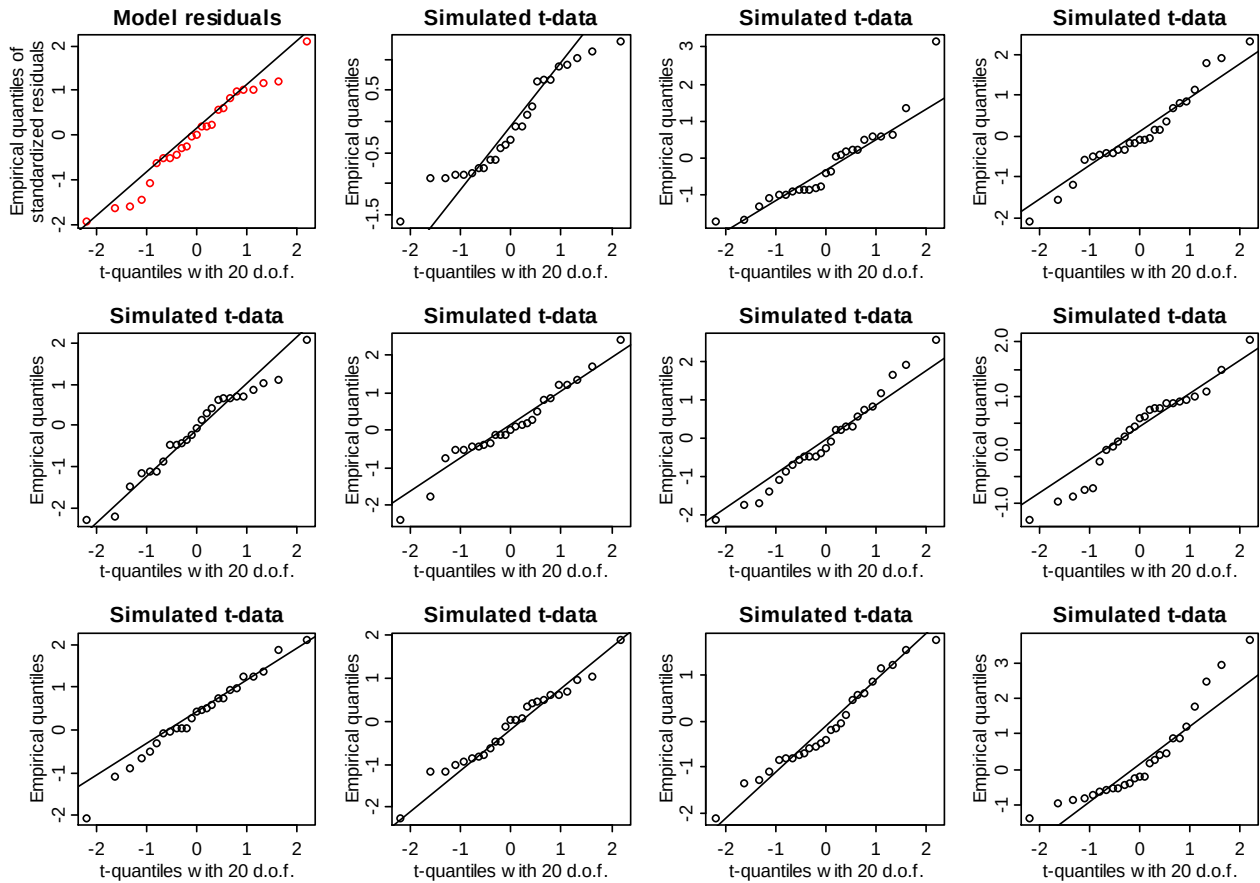


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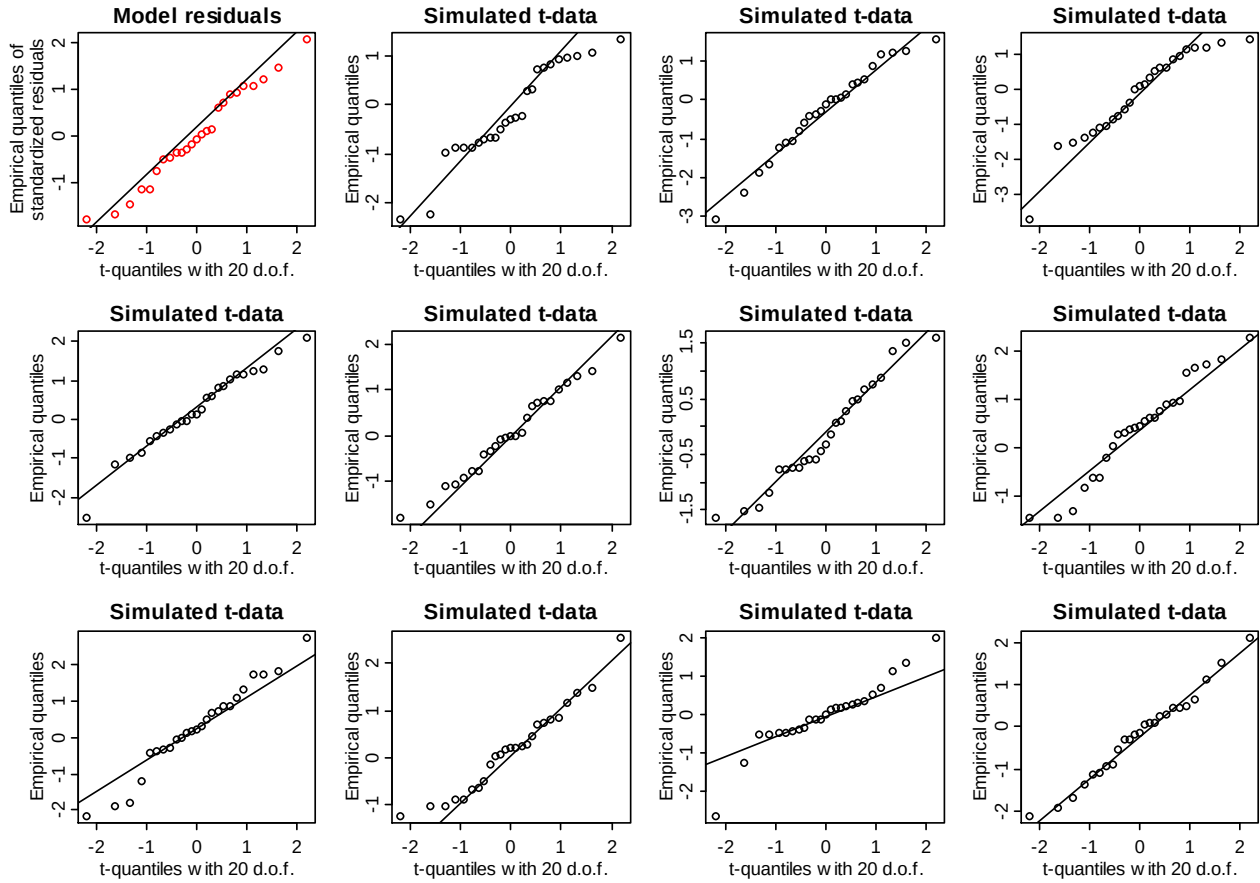


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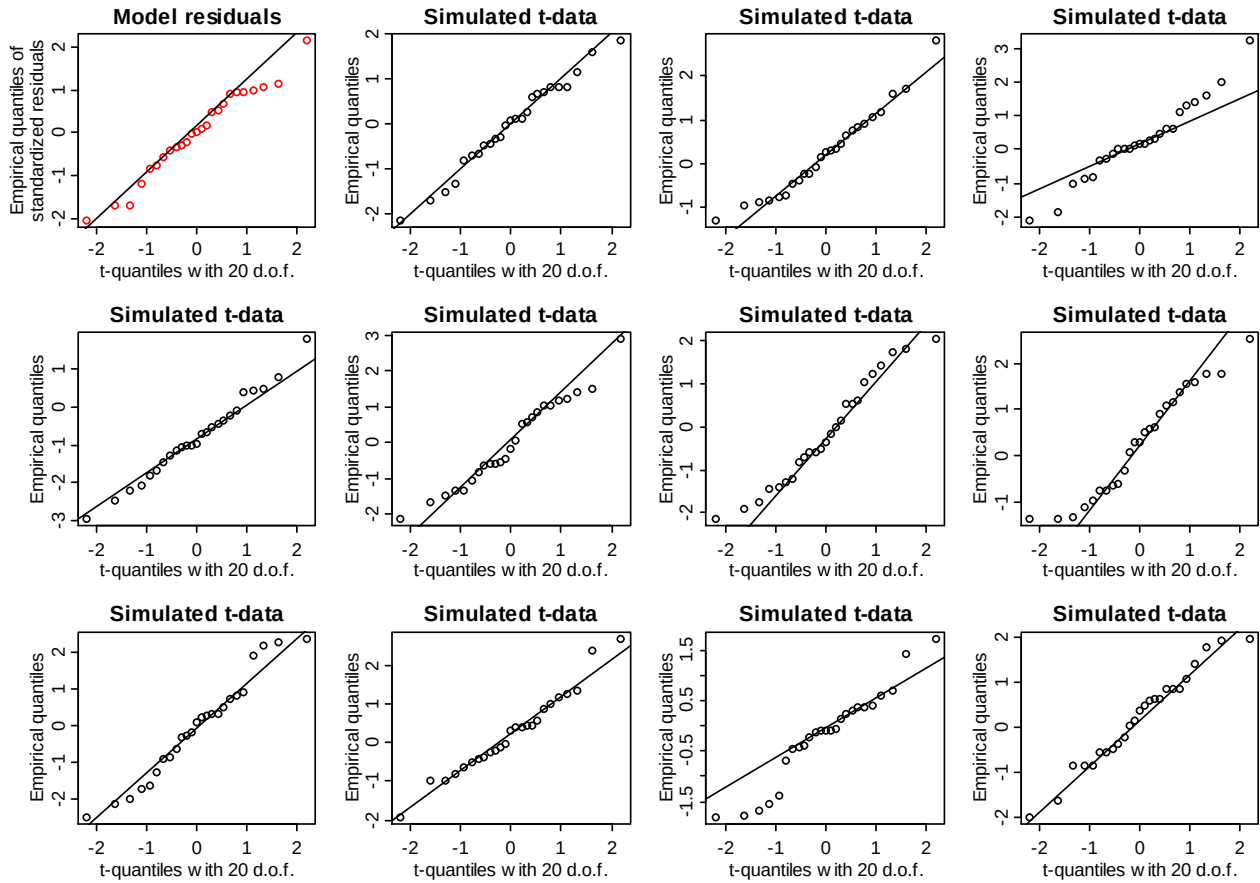


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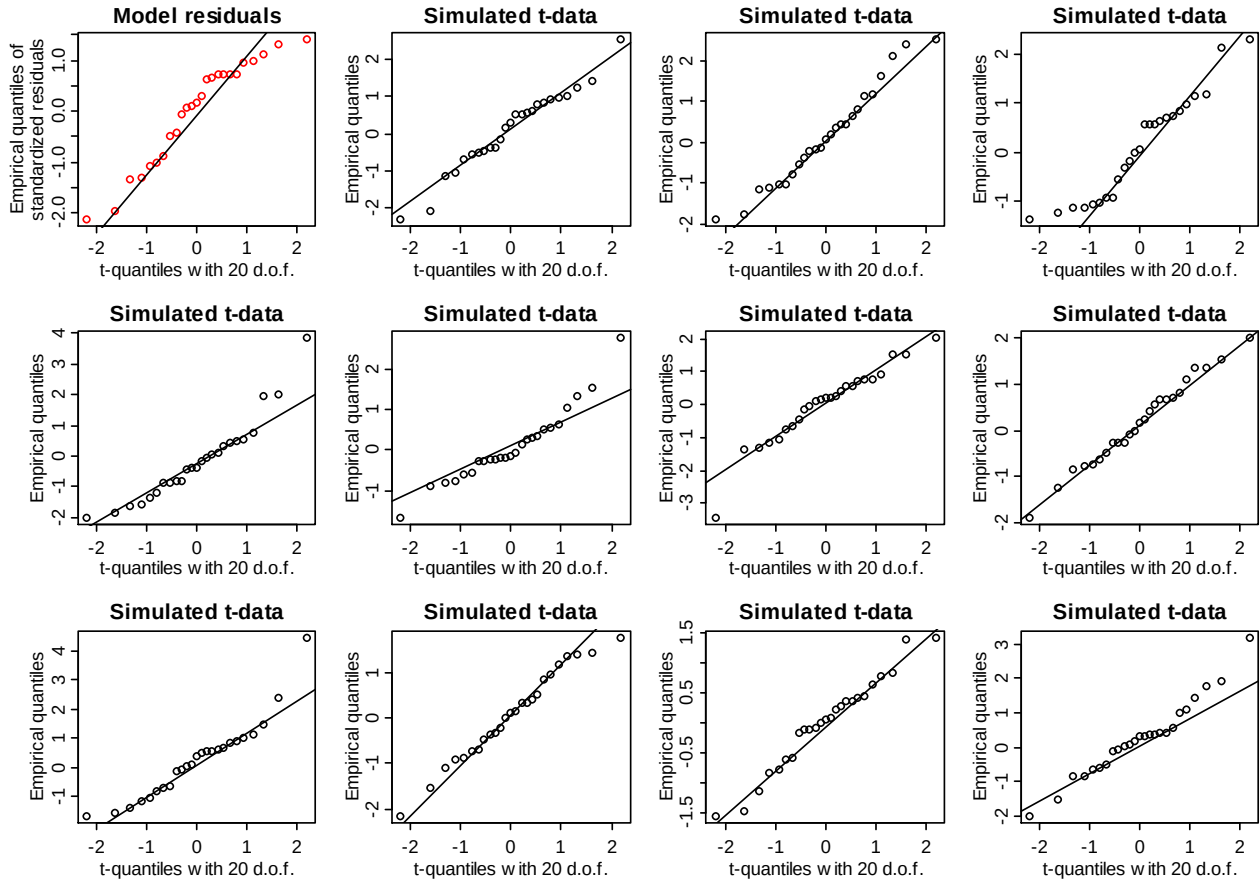


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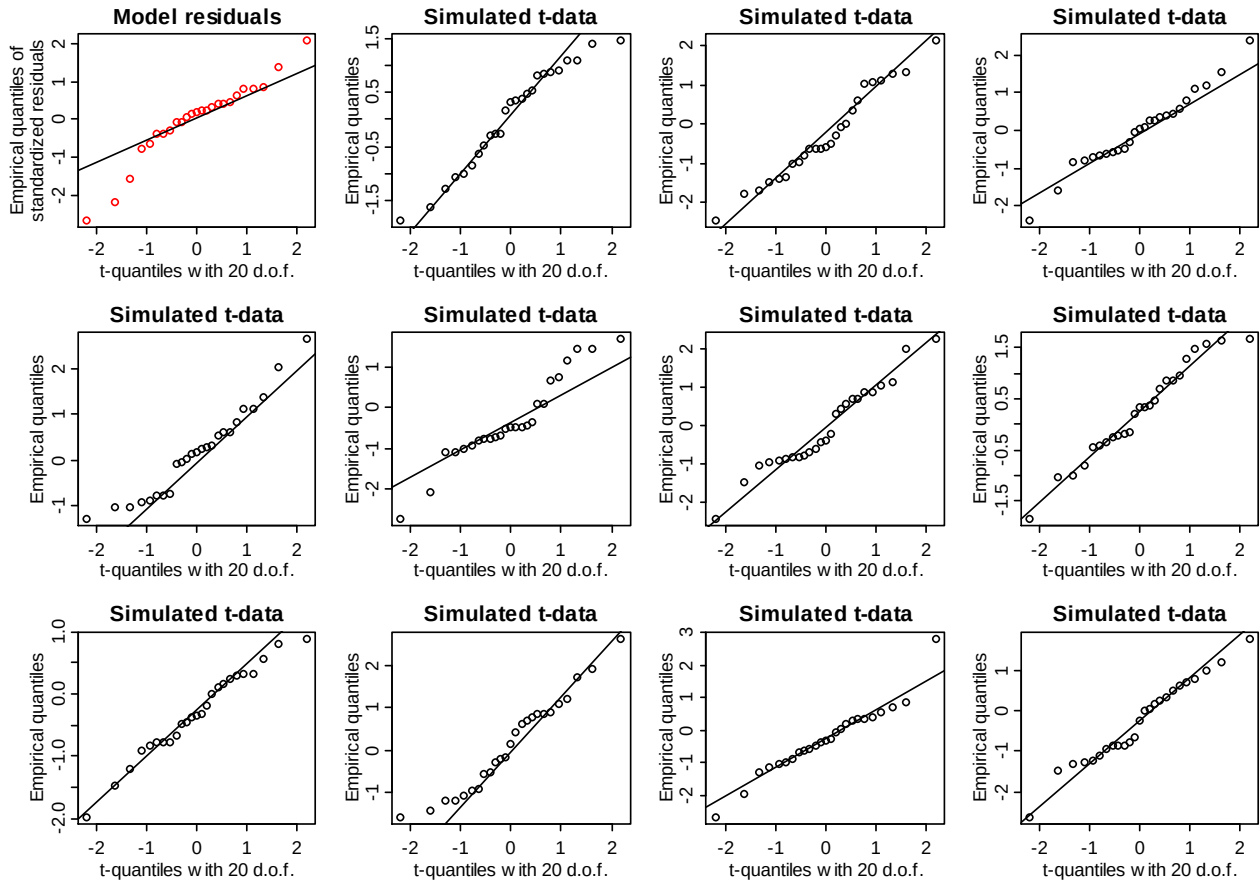


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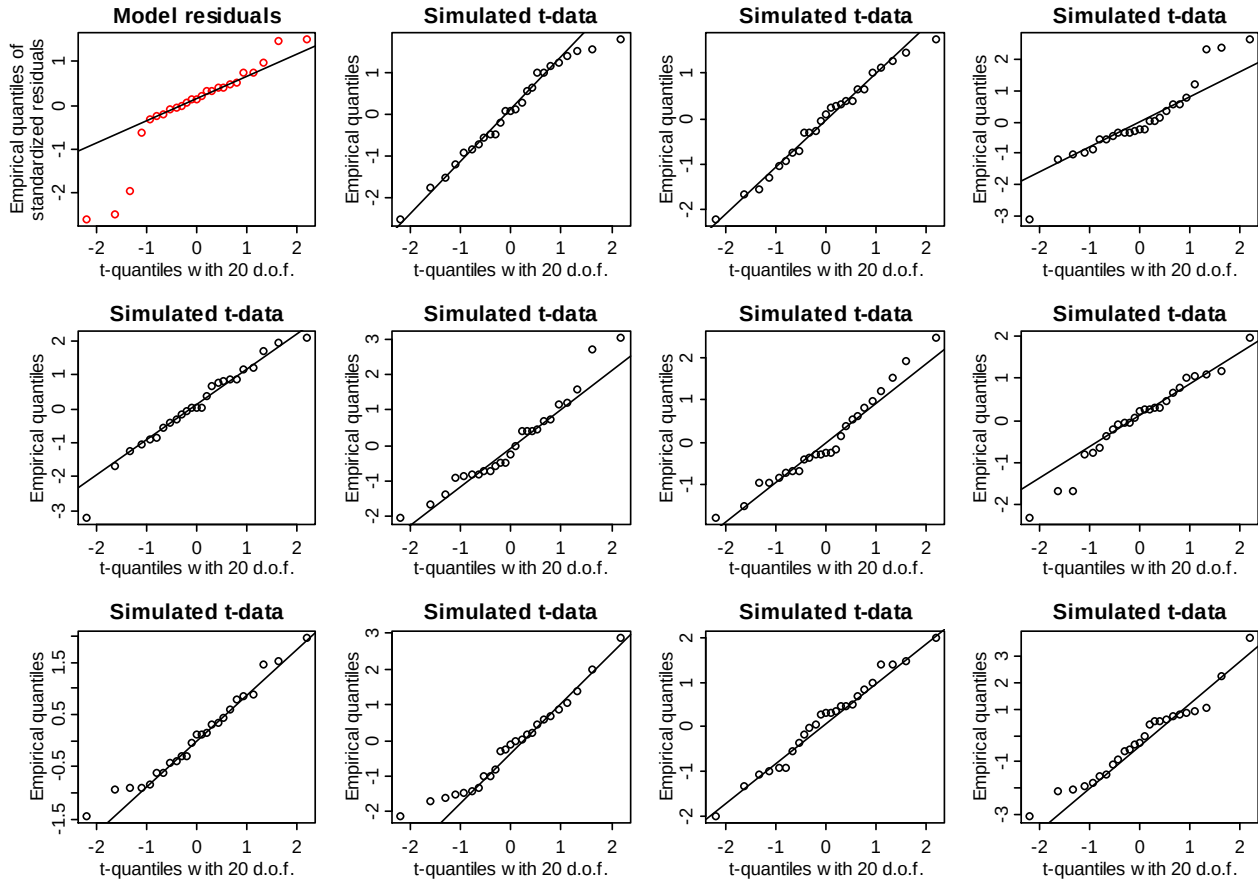


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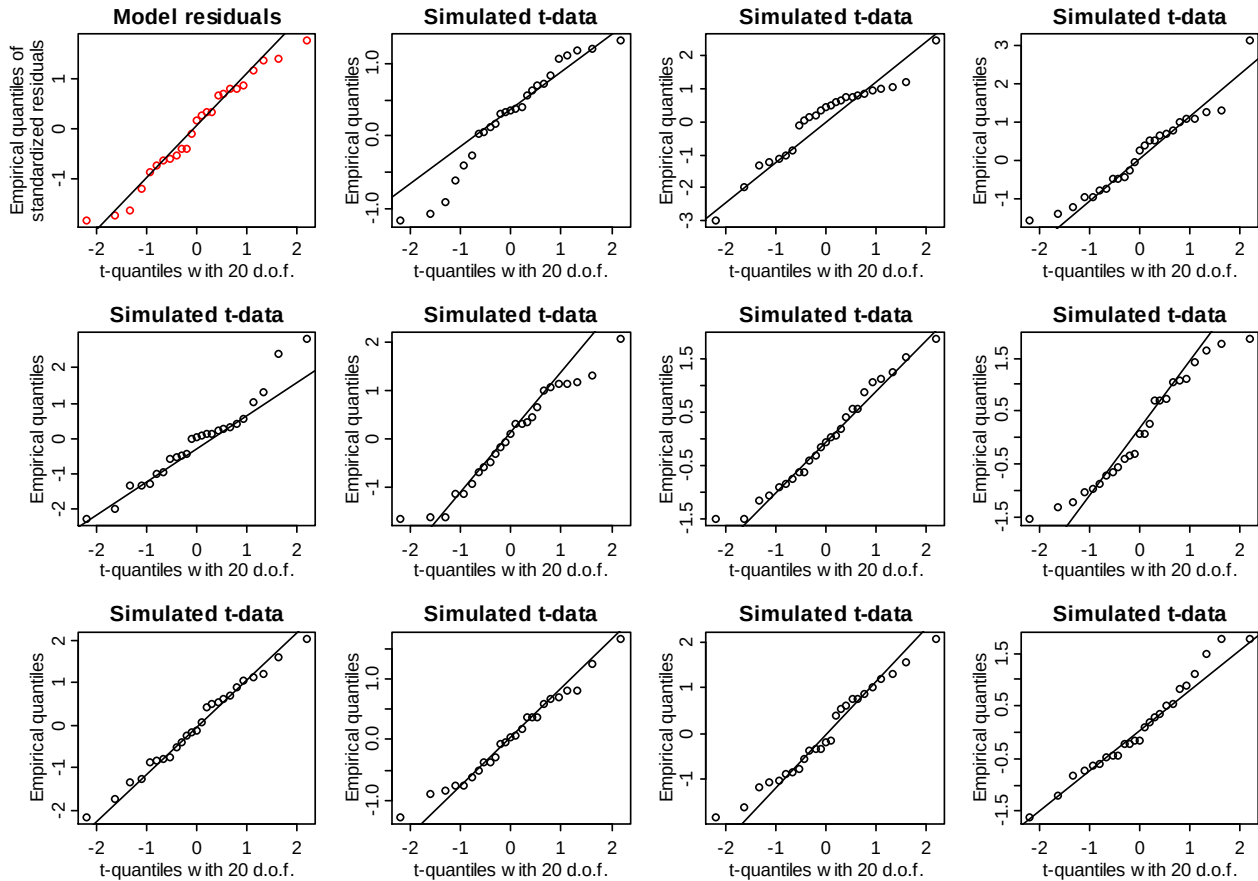


Figure S3 i

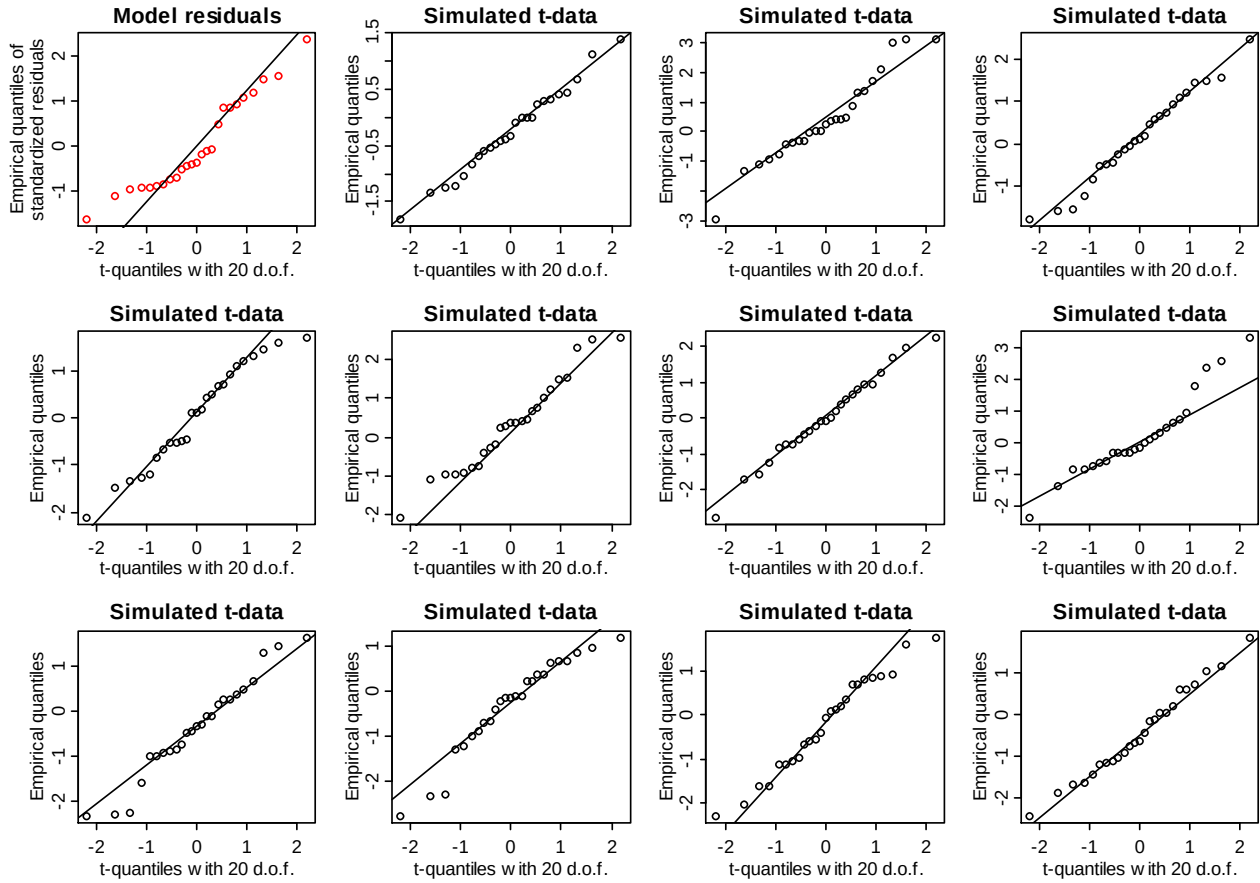


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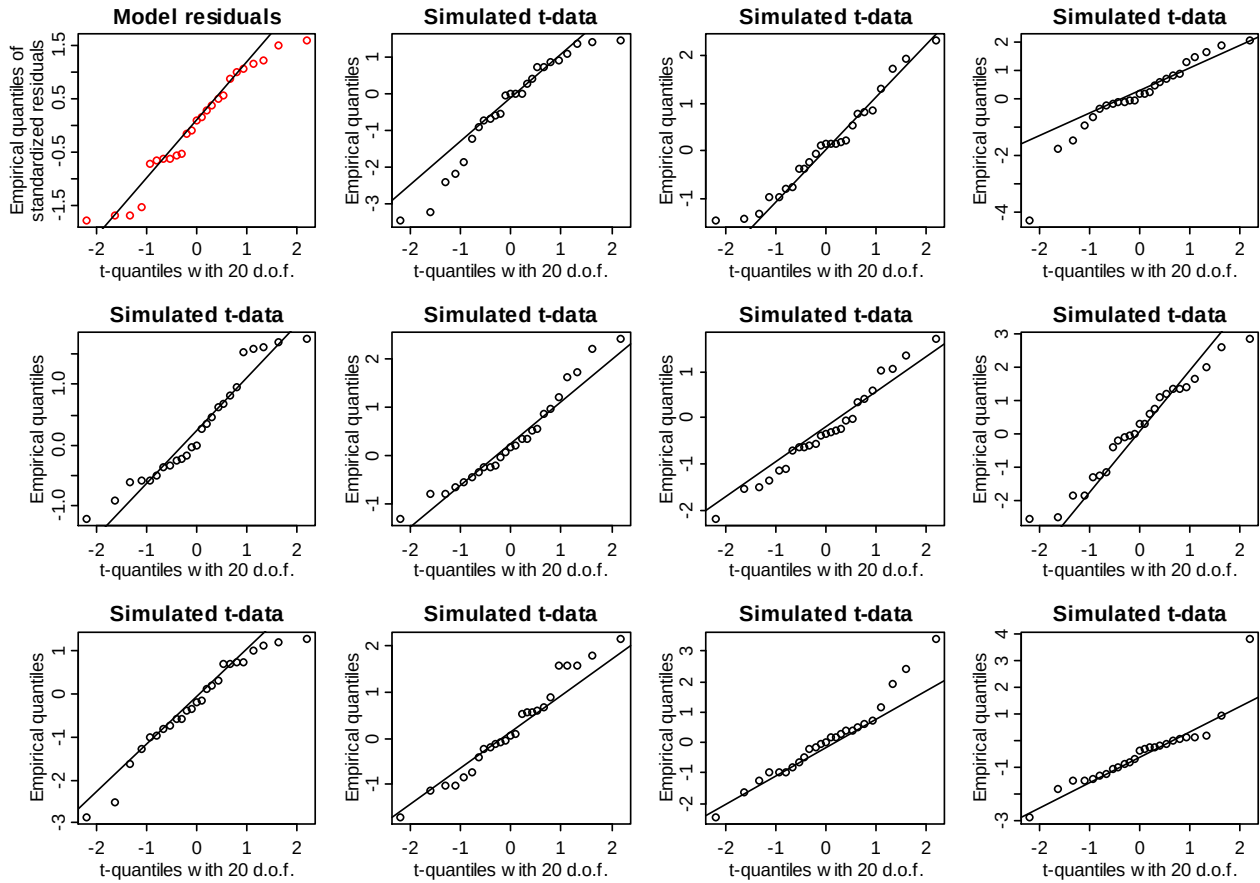


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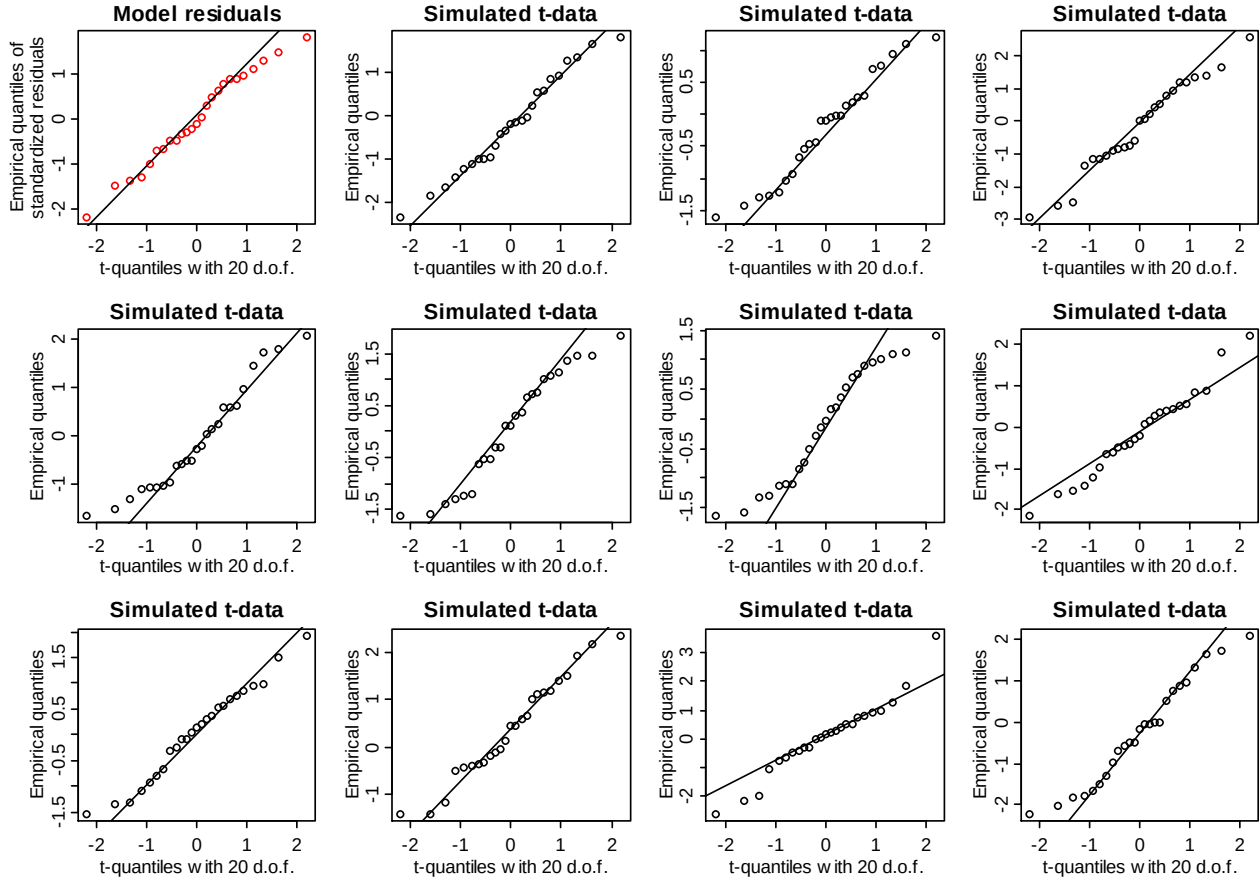


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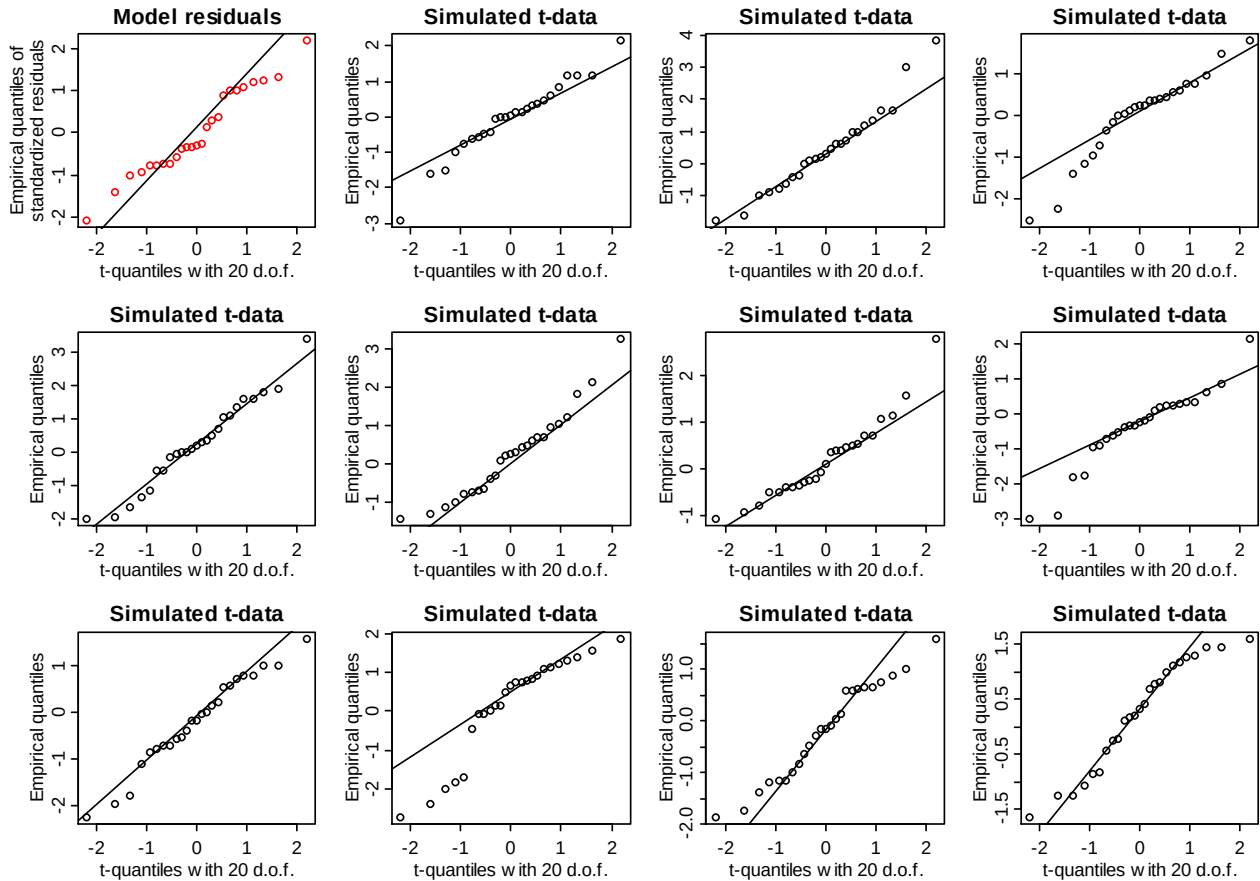


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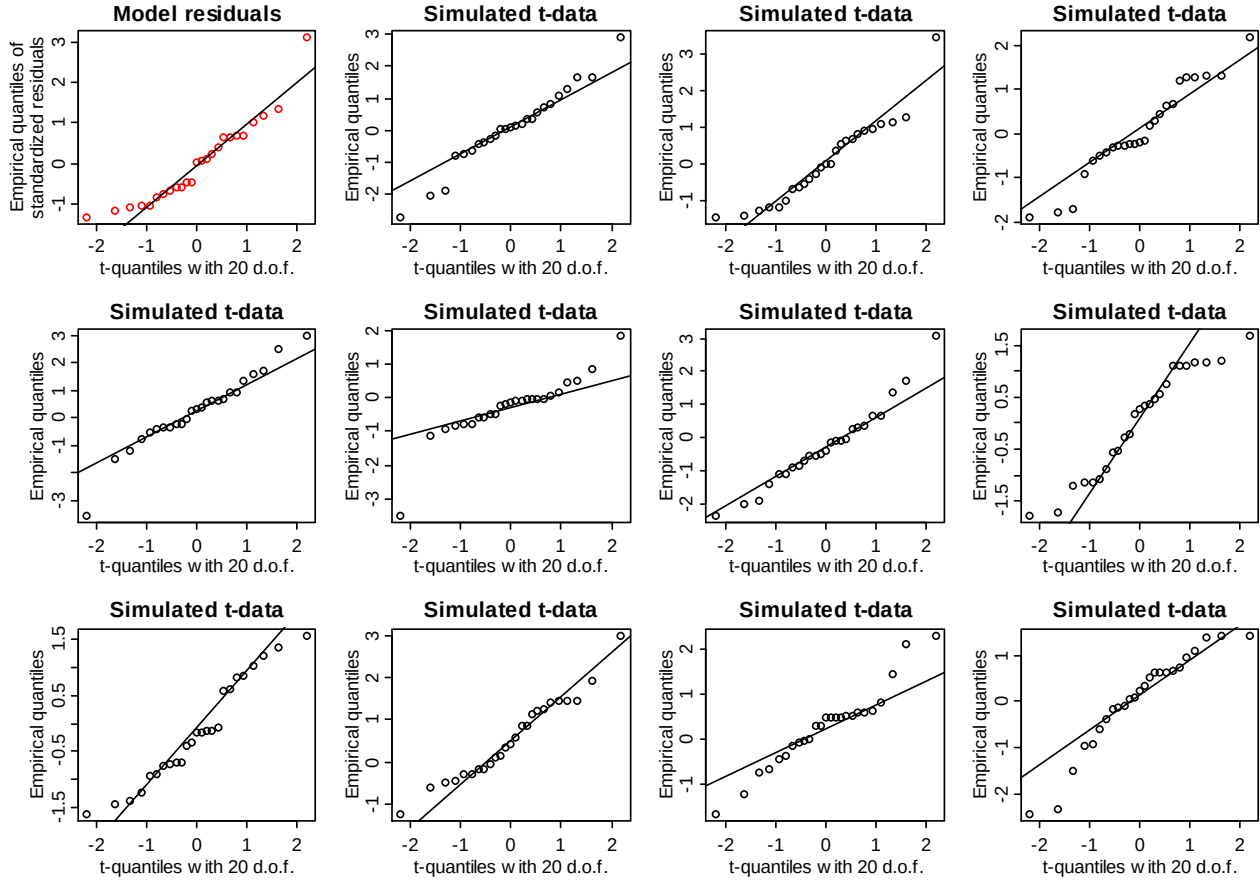


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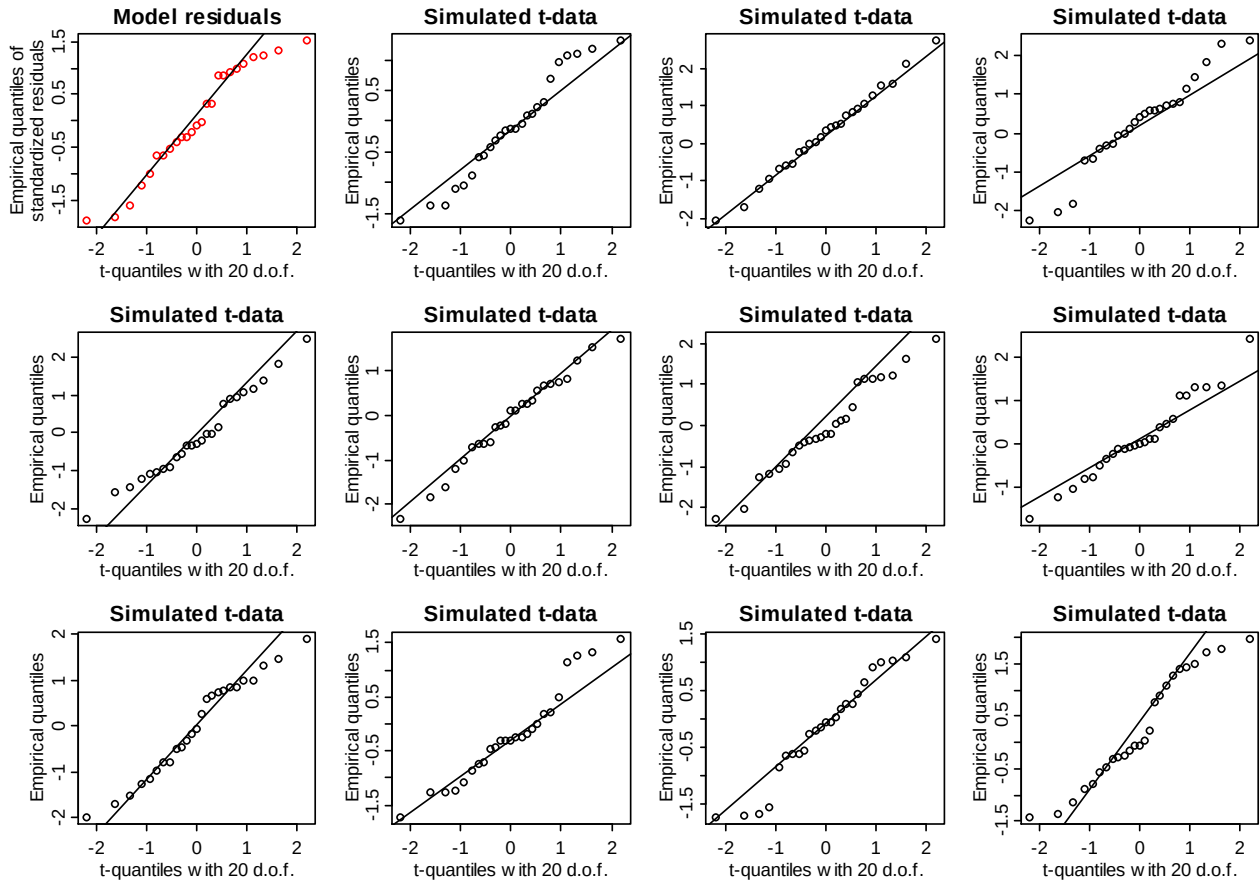


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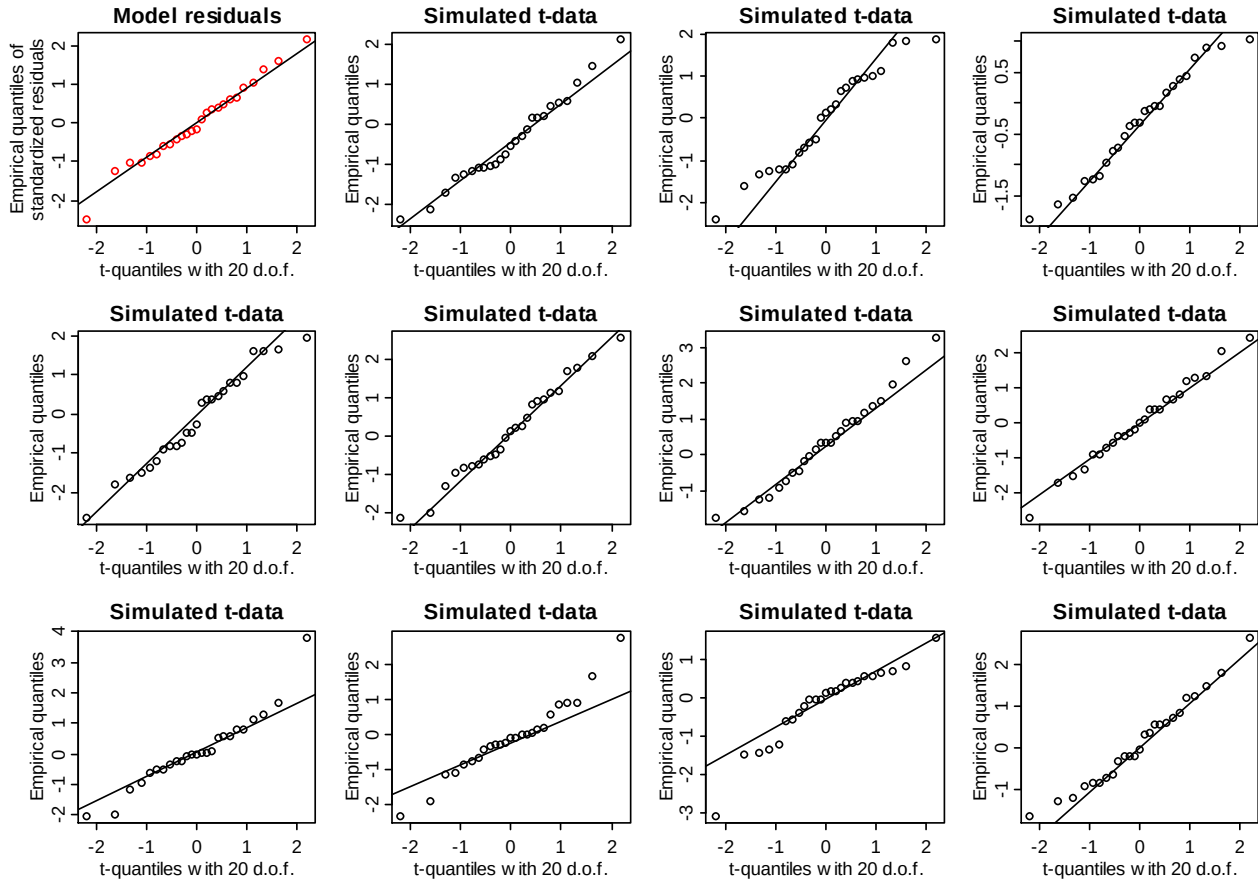


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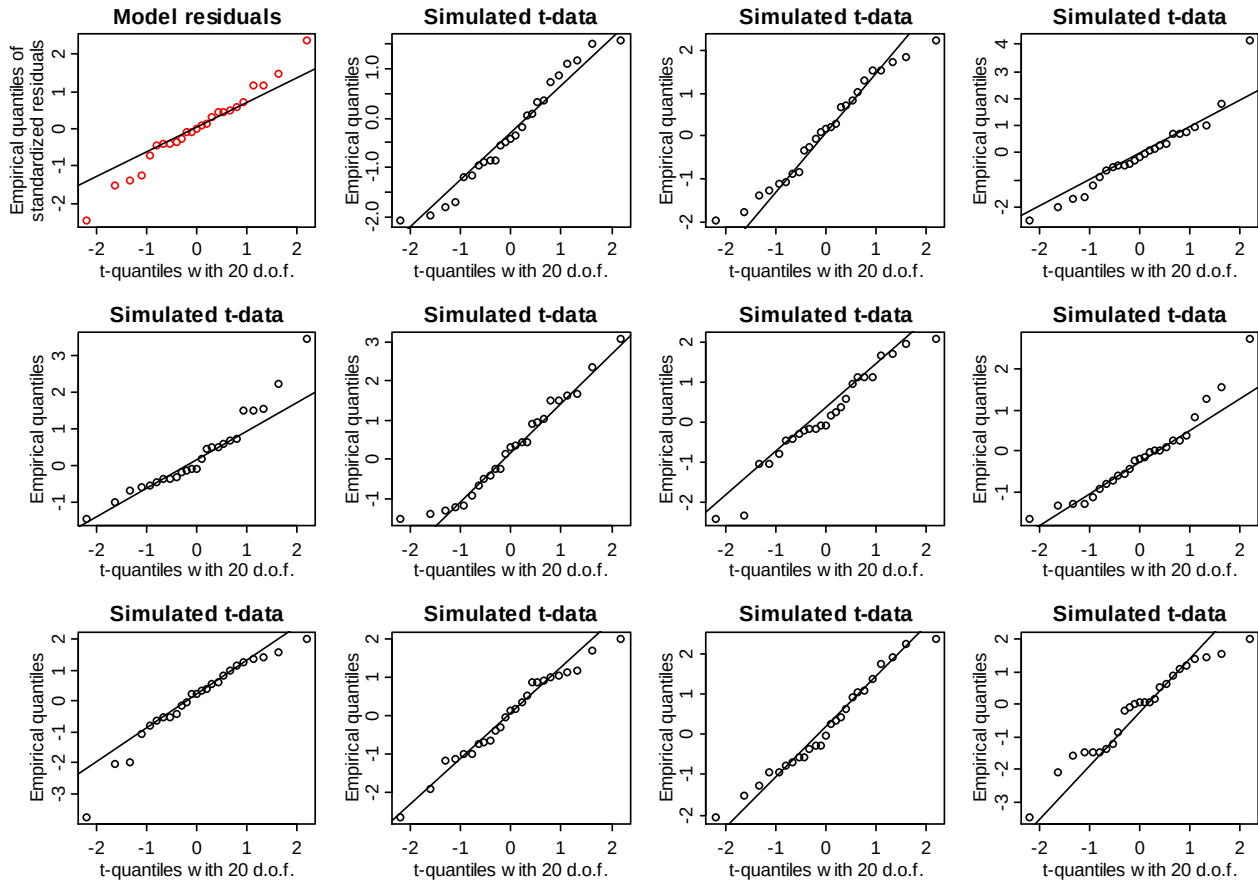


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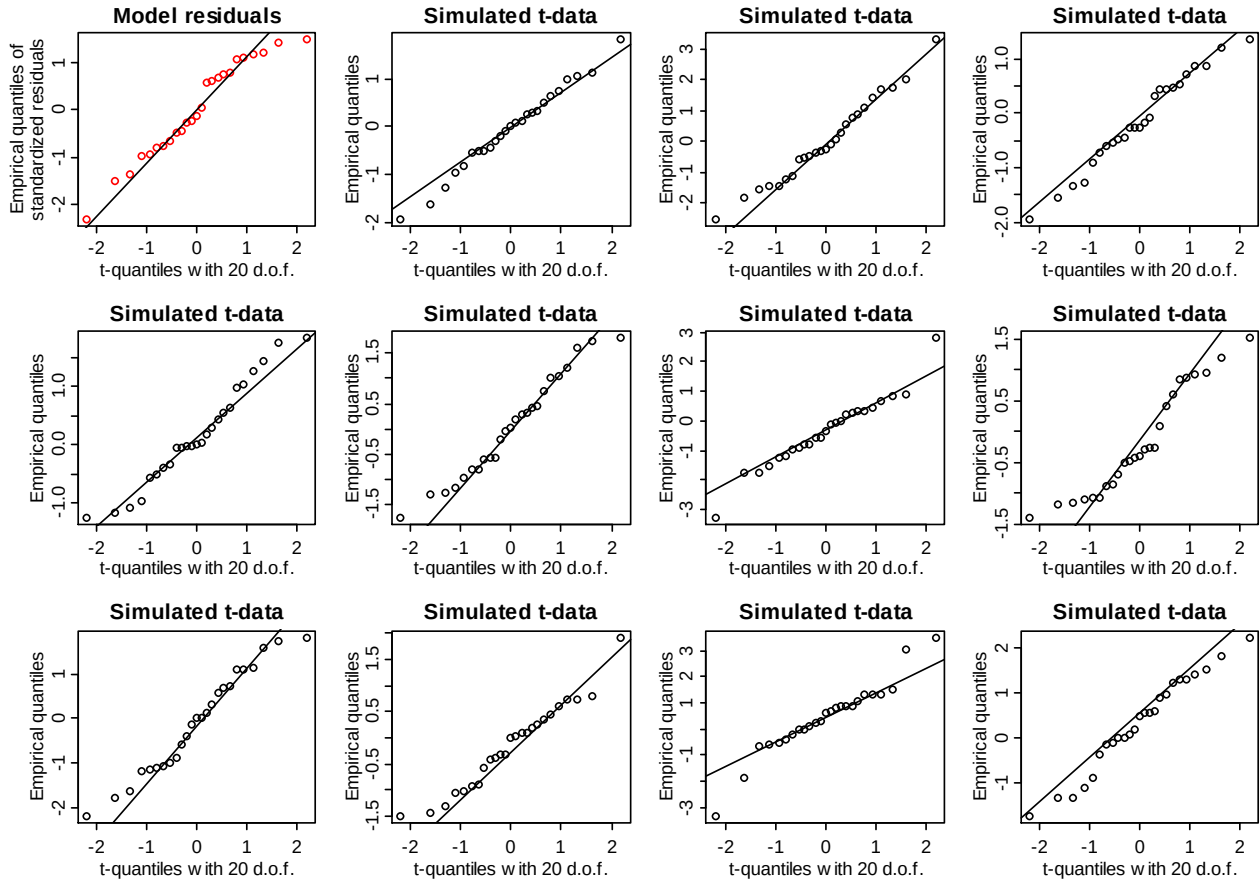


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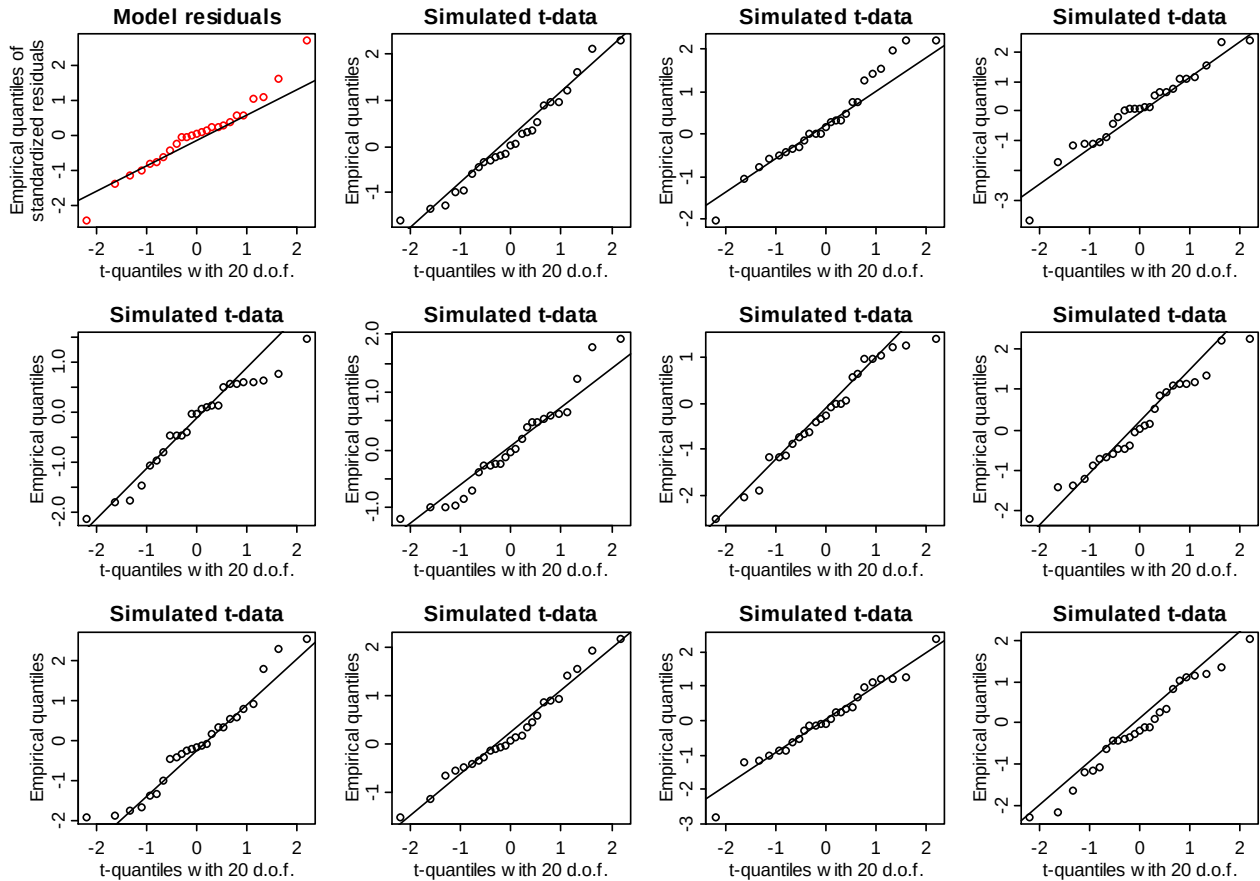


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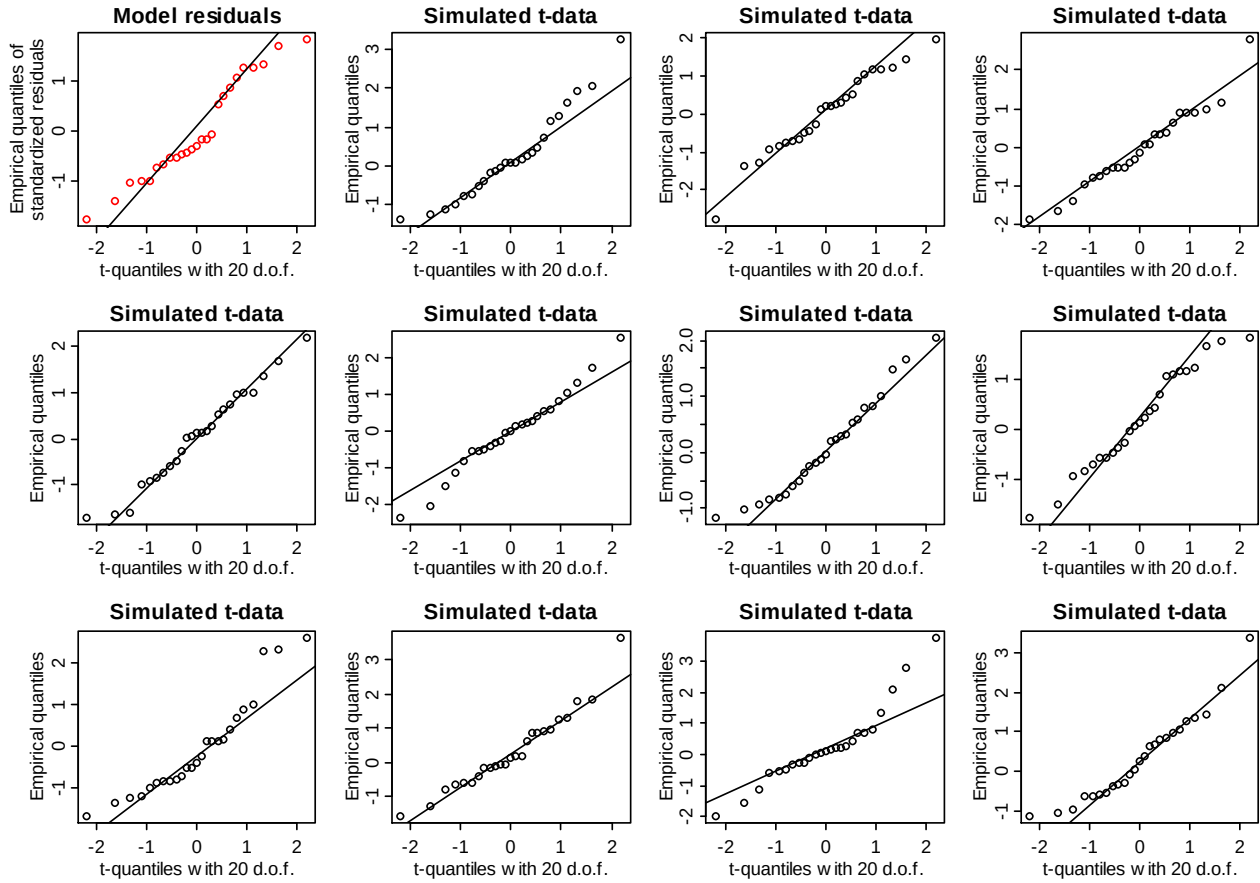


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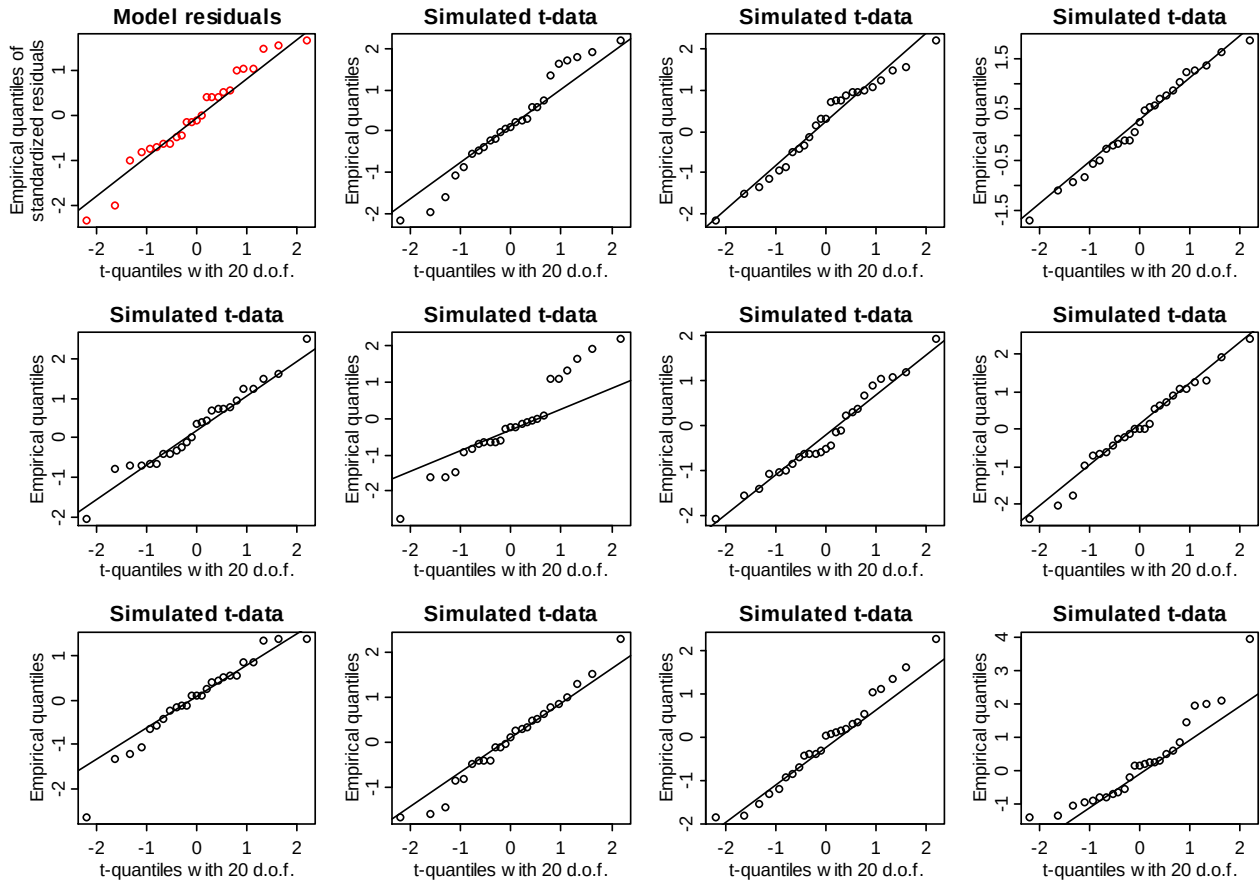


Figure S3 u

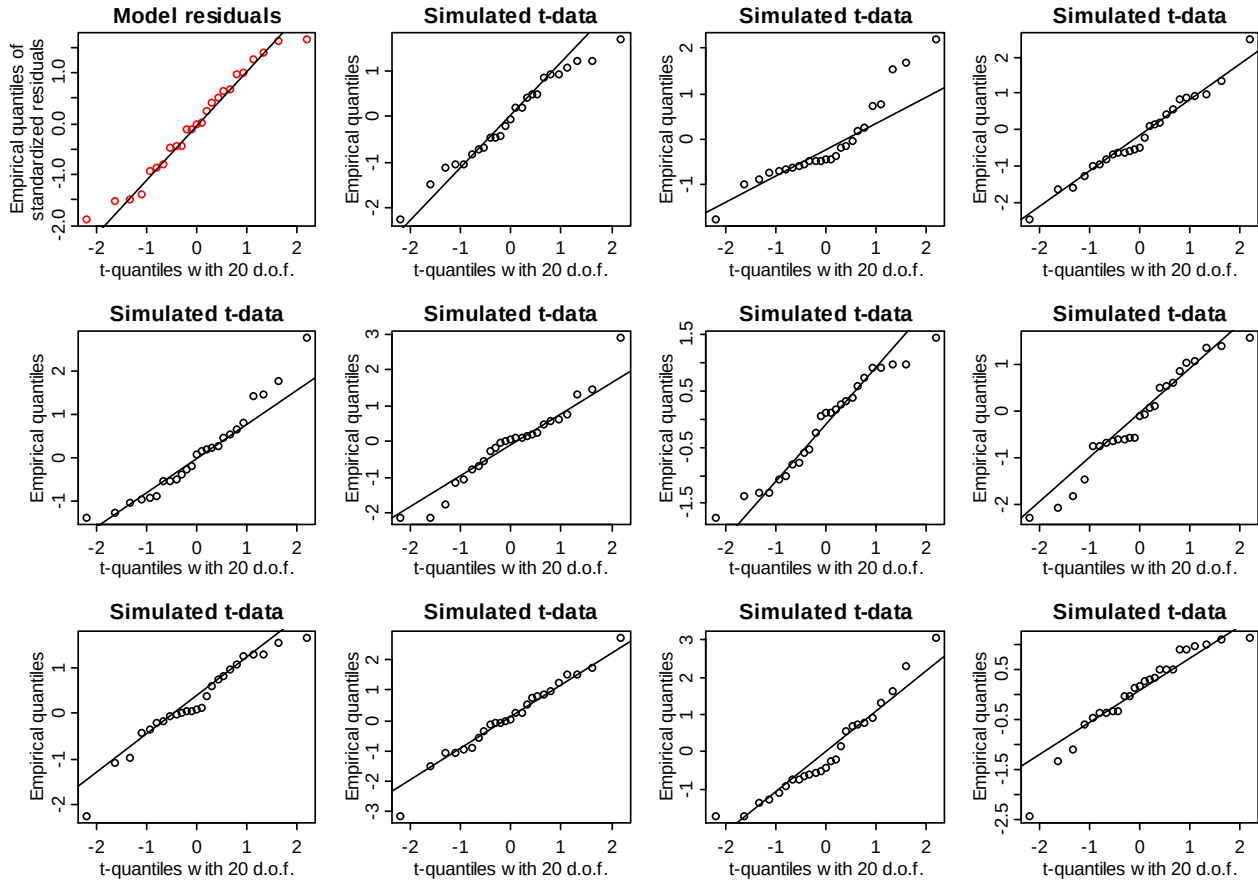


Figure S3 v

